

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd

OM protein - protein search, using sw model

Run on: January 16, 2003, 16:42:17 Search time 9 21:29 Seconds
(without alignments)
58.517 Million cell updates/sec

Title: US-09-856-070-26

Perfect score: 28

Sequence: 1 QDYEE 5

Scoring table: R10SNM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134122 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	28	100.0	130	2 H84133	hypothetical prote
2	28	100.0	156	2 H83825	hypothetical prote
3	28	100.0	253	2 A95223	hypothetical prote
4	28	100.0	253	2 C98987	oxidoreductase (EC
5	28	100.0	315	2 A56561	35K proline-rich p
6	28	100.0	339	2 I08677	hypothetical prote
7	28	100.0	361	2 D95106	conserved hypothet
8	28	100.0	361	2 F97974	conserved hypothet
9	28	100.0	385	2 C75020	tryptophanyl-tRNA
10	28	100.0	432	2 I13476	hypothetical prote
11	28	100.0	443	2 I10891	GDP dissociation i
12	28	100.0	505	2 C72064	glutamyl-tRNA synth
13	28	100.0	505	2 D66560	glutamyl-tRNA synth
14	28	100.0	512	2 F90124	t-complex protein
15	28	100.0	568	2 I05060	hypothetical prote
16	28	100.0	575	2 A96766	unknown protein P2
17	28	100.0	581	2 I45889	serin bovine
18	28	100.0	586	2 A34400	serin bovine
19	28	100.0	630	2 T47177	hypothetical prote
20	28	100.0	700	2 E84131	transcription anti
21	28	100.0	811	2 T40376	probable glutamyl
22	28	100.0	961	2 H86181	hypothetical prote
23	28	100.0	1188	2 D86311	protein P113.20 [I
24	28	100.0	1263	2 I15196	hypothetical prote
25	25	89.3	85	2 E82547	hypothetical prote
26	25	89.3	82	2 F64308	hypothetical prote
27	25	89.3	90	2 F82775	hypothetical prote
28	25	89.3	97	2 A72346	hypothetical prote
29	25	89.3	99	2 A11786	hypothetical prote

30	25	89.3	105	2 A82407	hypothetical prote
31	25	89.3	113	2 I41691	hypothetical prote
32	25	89.3	127	2 A91529	hypothetical prote
33	25	89.3	127	2 A71171	hypothetical prote
34	25	89.3	129	2 A98221	hypothetical prote
35	25	89.3	131	2 B96782	unknown protein P2
36	25	89.3	132	2 I17907	hypothetical prote
37	25	89.3	134	2 A44173	calcitonin gene-re
38	25	89.3	141	2 F64033	hypothetical prote
39	25	89.3	146	2 A63065	conserved hypothet
40	25	89.3	162	2 D69439	conserved hypothet
41	25	89.3	187	2 B79658	probable eip prote
42	25	89.3	187	2 H86974	elongation factor
43	25	89.3	190	2 H83689	hypothetical prote
44	25	89.3	200	2 T49472	hypothetical prote
45	25	89.3	201	2 D86488	hypothetical prote

ALIGNMENTS

RESULT 1

H84133

Hypothetical protein H83872 [imported] - Bacillus halodurans (strain C-125)

C.Species: Bacillus halodurans

C.Date: 01 Dec 2000 #sequence_revision 01 Dec 2000 #text_change 15-Jun-2001

C.Accession: H84133

R.Takami, H.: Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H

Nucleic Acids Res. 28, 4317-4331, 2000

A.Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans

A.Reference numbers: A83650; MUID:29512582; PMID:11058132

A.Accession: H84133

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-130 <STO>

A.Cross references: Jb.A901620; Gb.HA000004; NID:q10176401; P1IN:BA00591.1; GSPDB:G

A.Experimental source: strain C-125

C.Genetics:

A.Gene: BH3872

Query Match: 100.0%, Score 28, DB 2, Length 130;

Best Local Similarity: 100.0%; pred. No. 35;

Matches: 5; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 QDYEE 5

|||||

DB 81 QDYEE 85

RESULT 2

H83825

Hypothetical protein H81488 [imported] - Bacillus halodurans (strain C-125)

C.Species: Bacillus halodurans

C.Date: 01 Dec 2000 #sequence_revision 01 Dec 2000 #text_change 15-Jun-2001

C.Accession: H83825

R.Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H

Nucleic Acids Res. 28, 4317-4331, 2000

A.Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans

A.Reference numbers: A83650; MUID:29512582; PMID:11058132

A.Accession: H83825

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-156 <STO>

A.Cross references: Gb.A901620; Gb.HA000004; NID:q10176401; P1IN:BA00591.1; GSPDB:G

A.Experimental source: strain C-125

C.Genetics:

A.Gene: BH1408

Query Match:

Best Local Similarity: 100.0%; Score 28, DB 2, Length 156;

Matches: 5; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 QDYEE 5

Db 9 QVYEE 13
|||||

RESULT 3

A55223

hypothetical protein sp5589 [imported] - Streptococcus pneumoniae (strain T1634)

C:Species: Streptococcus pneumoniae

C:Date: 03-Aug-2001 #sequence_revision 03 Aug-2001 #text_change 24-Aug-2001

C:Accession: A55223

R:Jettellin, H.; Nelson, K.E.; Paulsen, K.E.; Read, J.A.; Peterson, S.; Hickey, T.; Hickey, E.K.; Holt, L.E.

on, J.D.; Umayam, L.A.; White, G.; Salzborg, S.L.; Lewis, M.P.; Radu, D.; Holtzapfel, Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris, A:Title: Complete Genome Sequence of a Virulent Isolate of Streptococcus pneumoniae

A:Reference number: A55000; MIM:21457209; PMID:11461916

A:Accession: A55223

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-253 <KUR>

A:Cross-references: GB:AE005672; PIDN:AAK75045.1; EMBL:U000000000; EMBL:U000000000

A:Experimental source: strain 11634

C:Genetics:

A:Gene: SP1909

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 100.0%; Score 28; DB 2; Length 253;

Best Local Similarity 100.0%; Pred. No. 75;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVYEE 5

|||||

Db 99 QVYEE 103

|||||

Db 99 QVYEE 103

|||||

Db 99 QVYEE 103

|||||

Db 99 QVYEE 103

|||||

Db 99 QVYEE 103

|||||

Db 99 QVYEE 103

|||||

Db 99 QVYEE 103

|||||

Db 99 QVYEE 103

|||||

Db 99 QVYEE 103

|||||

Db 99 QVYEE 103

|||||

Db 99 QVYEE 103

|||||

Db 99 QVYEE 103

|||||

Db 99 QVYEE 103

|||||

Db 99 QVYEE 103

|||||

Db 99 QVYEE 103

|||||

Db 99 QVYEE 103

|||||

Db 99 QVYEE 103

|||||

Db 99 QVYEE 103

|||||

Db 99 QVYEE 103

|||||

Db 99 QVYEE 103

|||||

Db 99 QVYEE 103

|||||

Db 99 QVYEE 103

|||||

Db 99 QVYEE 103

|||||

Db 99 QVYEE 103

|||||

Db 99 QVYEE 103

|||||

Db 99 QVYEE 103

|||||

Db 99 QVYEE 103

C:Accession: A56561; S27946
R:Reddy, B.A.; Kloc, M.; Etkin, L.D.
Mech. Dev. 39, 143-150, 1992
A:Title: The cloning and characterization of a localized maternal transcript in Xenopus
A:Reference number: A56561; MIM:1284029
A:Accession: A56561
A:Molecule type: mRNA
A:Residues: 1-315 <RED>
A:Cross-references: LMB:894959; NID:9214904; PIDN:AAK73157.1; PID:q144905
A:Experimental source: oocyte
A:Comment: mRNA extracted from NPH backbone (NPH:126632)
C:Superfamily: SH3 homology
F:260 367/Domain: SH3 homology <SH3>

Query Match 100.0%; Score 28; DB 2; Length 415;

Best Local Similarity 100.0%; Pred. No. 96;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVYEE 5

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

C:Accession: A56561; S27946
R:Reddy, B.A.; Kloc, M.; Etkin, L.D.
Mech. Dev. 39, 143-150, 1992
A:Title: The cloning and characterization of a localized maternal transcript in Xenopus
A:Reference number: A56561; MIM:1284029
A:Accession: A56561
A:Molecule type: mRNA
A:Residues: 1-315 <RED>
A:Cross-references: LMB:894959; NID:9214904; PIDN:AAK73157.1; PID:q144905
A:Experimental source: oocyte
A:Comment: mRNA extracted from NPH backbone (NPH:126632)
C:Superfamily: SH3 homology
F:260 367/Domain: SH3 homology <SH3>

Query Match 100.0%; Score 28; DB 2; Length 415;

Best Local Similarity 100.0%; Pred. No. 96;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVYEE 5

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

C:Accession: A56561; S27946
R:Reddy, B.A.; Kloc, M.; Etkin, L.D.
Mech. Dev. 39, 143-150, 1992
A:Title: The cloning and characterization of a localized maternal transcript in Xenopus
A:Reference number: A56561; MIM:1284029
A:Accession: A56561
A:Molecule type: mRNA
A:Residues: 1-315 <RED>
A:Cross-references: LMB:894959; NID:9214904; PIDN:AAK73157.1; PID:q144905
A:Experimental source: oocyte
A:Comment: mRNA extracted from NPH backbone (NPH:126632)
C:Superfamily: SH3 homology
F:260 367/Domain: SH3 homology <SH3>

Query Match 100.0%; Score 28; DB 2; Length 415;

Best Local Similarity 100.0%; Pred. No. 96;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVYEE 5

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Db 226 QVYEE 230

|||||

Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYEE 5
Db 123 QDYEE 127

RESULT 8

F97974 conserved hypothetical protein sp|8822 [imported] - Streptococcus pneumoniae (strain 66)

C.Species: Streptococcus pneumoniae

C.Date: 22-Nov-2001 #sequence_revision 22-Oct-2001 #text_change 22 Oct 2001

C.Accession: F97974

R.Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczyk, L.; Burgett, S.; DeHoff, B.S.; H

C, R.; LeBlanc, D.J.; Lee, J.; Leffkowitz, E.J.; Liu, J.; Matsushima, P.; McAbidin, S.; M

Y, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A.Authors: Yang, Y.; Young Dellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.P.

A.Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A.Reference number: A97872; MUID:21424245; PMID:11544234

A.Accession: F97974

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-361 <KUP>

A.Cross-references: GR-AB007317; PIRN-BAK09426 1; PIR-Q1545423; CSF08-0000174

C.Genetics:

A.Gene: spr0822

Query Match 100.0%; Score 28; DB 2; Length 361;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYEE 5
Db 123 QDYEE 127

RESULT 9

C75020

tryptophanyl-tRNA synthetase (trps) PAB1111 - Pyrococcus abyssi (strain Orsay)

C.Species: Pyrococcus abyssi

C.Date: 20-Aug-1999 #sequence_revision 29 Aug 1999 #text_change 29 Aug 2000

C.Accession: C75020

Ratonyi, S.; Grosz, G.

Submitted to the EMBL Data Library, July 1999

A.Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru

A.Reference number: A75001

A.Accession: C75020

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-385 <KAW>

A.Cross-references: GR-A1248288; GR-A1098846; NID:q5458990; PIRN-CAH50601.1; PIR:q545911

A.Experimental source: strain Orsay

C.Genetics:

A.Gene: trps, PAB1111

C.Superfamily: mammalian tryptophan tRNA ligase amino acid-tRNA ligase repeat homology;

Query Match 100.0%; Score 28; DB 2; Length 385;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYEE 5
Db 66 QDYEE 70

RESULT 10

143476

hypothetical protein WPFP434082.1 human

C.Species: Homo sapiens (man)

C.Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000

C.Accession: T43476

R.Ansorge, W.; Winkler, H.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

Submitted to the Protein Sequence Database, December 1999

A.Reference number: Z22518

A.Accession: T43476

A.Status: preliminary

A.Molecule type: mRNA

A.Residues: 1-432 <AAA>

A.Cross-references: EMBL:AL133598

A.Experimental source: adult testis, clone DKFZp434H052

C.Genetics:

A.Note: WPFP434H052.1

C.Superfamily: human hypothetical protein WPFP434H052.1

Query Match 100.0%; Score 28; DB 2; Length 432;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYEE 5
Db 379 QDYEE 383

RESULT 11

T10801

GDP dissociation inhibitor GDI1 - Volvox carterii f. naqariensis

C.Species: Volvox carterii f. naqariensis

C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000

C.Accession: T10801

R.Heyser, K.; Fabry, S.

Submitted to the EMBL Data Library, July 1996

A.Description: Identification and characterization of a lower plant Ypt/Rab guanine

A.Reference number: Z17156

A.Accession: T10801

A.Status: preliminary; translated from GR/EMBL/DDRJ

A.Molecule type: mRNA

A.Residues: 1-443 <BEY>

A.Cross-references: EMBL:U62866; NID:q1572517; PIR:q1572518

A.Experimental source: strain HK10

C.Genetics:

A.Gene: GDI1

C.Function:

A.Description: inhibits dissociation of GDP from GTP binding proteins

C.Superfamily: human GTP dissociation inhibitor XAF-4

Query Match 100.0%; Score 28; DB 2; Length 443;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYEE 5
Db 147 QDYEE 151

RESULT 12

C72064

glutamate-tRNA ligase (EC 6.1.1.17) [similarity] - Chlamydomonas reinhardtii (strains

C.Species: Chlamydomonas reinhardtii [similarity]

C.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 03-Jun-2002

C.Accession: C72064; D81603

R.Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Glininger, L.; Grimwood,

Nature Genet. 21, 385-389, 1999

A.Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A.Reference number: A72060; MUID:99206606; PMID:10392388

A.Accession: C72064

A.Molecule type: DNA

A.Residues: 1-505 <ARN>

A.Cross-references: GR-AB001640; GR-AB001640; NID:q478845; PIRN-AAU18700.1; PIR:q437

A.Experimental source: strain C7L029

R.Kead, R.D.; Brunham, R.C.; Shen, C.; Gill, S.P.; Heideberg, J.F.; White, O.; Hicke

C. Eadsen, P.; Gwin, M.; Nelson, W.; LeRoy, E.; Kohnen, J.; McCarthy, G.; Saizbo

Nucleic Acids Res. 28, 1397-1406, 2000

A.Title: Genome sequence of Chlamydia trachomatis M 70 and Chlamydia pneumoniae AB-99

A.Reference number: A81606; MUID:20150255; PMID:10684935

A:Accession: DB1603
 A:Molecule type: DNA
 A:Residues: 1-505 <REA>
 A:Cross-references: GB:AE002180; GB:AE002161; PIDN:q7189117; PIDN:AAF38063.1; PID:q718912
 A:Experimental source: strain AP49, HL cells
 C:Genetics:

A:Gene: q1TX; CP0190

C:Superfamily: glutamate-tRNA ligase; glutamine-tRNA ligase homology
 C:Keywords: aminacyl-tRNA synthetase; ligase; protein biosynthesis
 F:6-420/domain: glutamine-tRNA ligase homology /ES2

Query Match: 100.0%; Score 28; DB 2; Length 505;
 Best Local Similarity: 100.0%; Pred. No. 1.6e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYEE 5

DB 54 QDYEE 58

RESULT 14

DB6560

glutamy-tRNA synthetase [imported] Chlamydomonas pneumoniae (strain J138)

C:Species: Chlamydomonas pneumoniae, Chlamydia pneumoniae

C:Date: 02 Mar 2001 #sequence_revision 02 Mar 2001 #text_change 23 Mar 2001

C:Accession: DB6560

R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ishiura, H.

Nucleic Acids Res. 28, 2311-2314, 2000

A:Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.

A:Reference number: A86491; MUID:20330349; PMID:10871362

A:Accession: DB6560

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-505 <STO>

A:Cross-references: GB:BA000008; MID:q8978941; PIDN:BAAG8766.1; GSPDB:GN00142

A:Experimental source: Strain J138

C:Genetics:

A:Gene: q1TX

C:Superfamily: glutamate-tRNA ligase; glutamine-tRNA ligase homology

Query Match: 100.0%; Score 28; DB 2; Length 505;

Best Local Similarity: 100.0%; Pred. No. 1.6e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYEE 5

DB 54 QDYEE 58

RESULT 14

F90124

t complex protein eta S0 [imported] - Giardia theta nucleomorph

C:Species: nucleomorph Giardia theta

A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24 May 2001

C:Accession: F90124

R:Antonius, S.; Zoller, S.; Frankholz, M.; Beaton, M.; Penny, S.; Dend, L.T.; Wu, X.; Ren

Nature 410, 1091-1096, 2001

A:Title: The highly reduced genome of an enslaved algal nucleus.

A:Reference number: A99082; MUID:11423671; PMID:11323671

A:Accession: F90124

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-512 <GOI>

A:Cross references: GB:AF084041; MID:q1479444; PIDN:AAK39691.1; GSPDB:GN00152

C:Genetics:

A:Gene: teph

A:Map position: 3

A:Genome: nucleomorph

C:Keywords: nucleomorph

Query Match

Best Local Similarity: 100.0%; Score 28; DB 2; Length 512;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYEE 5

DB 78 QDYEE 82

RESULT 15

T05060

hypothetical protein M3E9.130 Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun 1999

C:Accession: T05060

R:Hevar, M.; Vandenbol, M.; Jallet, C.; Portetelle, D.; Boelsel, J.; Mewes, H.W.; Ma

submitted to the Protein Sequence Database, March 1999

A:Reference number: Z15396

A:Accession: T05060

A:Molecule type: DNA

A:Residues: 1-568 <BEV>

A:Cross-references: PMBL:AI022223

A:Experimental source: cullivar Columbia; BAC clone M3E9

C:Genetics:

A:Map position: 4

A:Insertions: 105/3; 335/2; 392/2

A:Note: M3E9.130

Query Match

Best Local Similarity: 100.0%; Score 28; DB 2; Length 568;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYEE 5

DB 157 QDYEE 161

Search completed: January 16, 2003, 16:57:54

Job time: 9.21429 secs